

## REMARKS

### 1. Formal Matters

#### a. Status of the Claims

Claims 25-27, 29-31, and 33 are pending in this application. Claims 26, 29, 30, and 33 have been withdrawn from consideration. Claim 27 is hereby canceled without prejudice to pursuing the canceled subject matter in a continuing application. Claims 25 and 31 are amended, and claims 34 and 35 are new. Applicant respectfully requests entry of the amendments and remarks made herein into the file history of this application. Upon entry of the amendments, claims 25, 26, 29-31, and 33-35 will be pending, and claims 25, 31, 34, and 35 will be under active consideration.

#### b. Amendments to the Claims

Claim 25 is amended to add language that the nucleic acid “consists of a sequence” selected from the group recited in parts (a)-(d). Applicant requests this amendment for clarification purposes only—it does not affect the scope of the claim.

Claim 31 is amended to no longer depend from claim 27. This claim is also amended to clarify its scope in order to expedite prosecution. Other than removing its dependency from claim 27, none of the amendments to claim 31 changes its scope.

Support for new claim 34 can be found at paragraphs 0026, 0507, 0518 and 0519 of the specification as originally filed.

Support for new claim 35 can be found in the specification as originally filed at paragraphs 0042 and 0046.

#### c. Interview Summary

Applicant would like to thank Examiner Wollenberger for the courtesy of holding the telephone interviews on October 23, 2008 and October 29, 2008 with Teddy C. Scott, Jr., during which the utility rejection was discussed.

#### d. Objection under 37 C.F.R. § 1.75(c)

On page 3 of the Office Action, the Examiner objects to claim 31 under 37 C.F.R. § 1.75(c) as allegedly being of improper dependent form. The Examiner interprets the scope of independent claim 25 to be limited to the sequences set forth in parts (a)-(c)[sic]. Claim 31 is related to a vector comprising a nucleic acid of claim 25. The Examiner is correct that claims drawing their dependency from an independent claim must contain all the limitations of the independent claim and can only further limit the subject matter of the independent claim. The Examiner, however, has misconstrued the scope of vector claim 31 by impermissibly expanding the scope of independent nucleic acid claim 25 beyond its

limitations and therefore, in turn, expanding the scope of vector claim 31 beyond its permissible limitations.

Specifically, the Examiner alleges that the vector may comprise long stretches of DNA encoding the nucleic acid of part (a) along with any other additional RNA sequences. This interpretation is in stark contrast to the Examiner's correct acknowledgment that the scope of independent claim 25 is directed to nucleic acids consisting of sequences set forth in (a)-(d). Accordingly, if dependent vector claim 31 must contain the limitation of claim 25, the vector must comprise an insert consisting of the nucleic acid of claim 25 wherein the vector does not comprise any other inserts but the nucleic acid of claim 25. Of course, the vector of claim 31 would contain unrecited elements familiar to one of skill that allow the vector to properly function (*e.g.*, replicates, *etc.*) or have a particular characteristic (*e.g.*, antibiotic resistance, multiple cloning site, *etc.*), but these unrecited elements would not be sequences within the insert of claim 25. However, the vector of claim 31 would not include an insert with additional sequences such as the 253,070 extraneous nucleotides of GenBank Accession No. AC\_09504.7 (as cited by the Examiner below), which allegedly harbors SEQ ID NO: 7002375. Such an insert of GenBank Accession No. AC\_096504.7 would not be within the scope of vector claim 31 because the insert would be outside the scope of claim 25. Accordingly, claim 31 contains all the limitations of claim 25 and does not impermissibly expand its scope to include unrecited elements, and in fact, limits the vector insert to nucleic acids of claim 25.

In order to expedite prosecution, claim 31 is amended to clarify that the vector may not comprise a human insert that falls outside the scope of claim 25. Applicant submits that the scope of the claim is not changed by the amendment. Applicant notes that the scope of instant claims 31 and 34 is not limited to including only one copy of an insert consisting of a nucleic acid falling within the scope of claim 25. Nor is the scope of instant claims 31 and 34 limited to one particular nucleic acid that falls within the scope of claim 25. In view of the foregoing, Applicant submits that vector claim 31 properly includes all the limitations of claim 25 by only requiring an insert consisting of the nucleic acid of claim 25.

## **2. Patentability Remarks**

### **a. 35 U.S.C. § 101 and 112, first paragraph**

On page 4 of the Office Action, the Examiner rejects claims 25, 27, and 31 under 35 U.S.C. § 101 for allegedly lacking a credible asserted utility. The Examiner acknowledges a credible utility for the 22-nucleotide miRNA encoded by SEQ ID NO: 7002375, the DNA encoding this miRNA, the complement of the miRNA and DNA, and the vector comprising these nucleic acids. *The Office Action*, at p. 4.

The Examiner maintains his rejection of claimed subject matter related to sequences that are 80% identical to SEQ ID NO: 7002375, as well as any complements thereof with less than 100% identity to SEQ ID NO: 7002375. The Examiner asserts that Applicant has not provided evidence that addresses the

proposed activities of sequences less than 100% identical to the miRNA. However, Applicant submits that the Examiner has failed to consider that SEQ ID NO: 7002375 is not 100% complementary to its target sequence. Shown below is a depiction of the interaction between the miRNA having SEQ ID NO: 7002375 (bottom strand) and its target sequence MAPKAPK2 (top strand). This interaction is disclosed in Table 7A of the application as originally filed.

	T G	- GA---
MAPKAPK2	A A GAG T	GTGTATGT
SEQ ID NO: 7002375	T T CTC A	CACATACA
	T T	C AAGGG

The depiction shows that fourteen out of twenty-two nucleotides (63.4%) of the miRNA are complementary with its target sequence. The Examiner has failed to provide any basis for his contention that sequences less than 100% identical to the miRNA would not be expected to affect expression of the target. Accordingly, Applicant submits that the subject matter claimed in claim 25 has a credible utility, and therefore respectfully requests that the Examiner reconsider and withdraw the rejection of the claims under 35 U.S.C. § 101.

**b. 35 U.S.C. § 112, second paragraph**

On page 6 of the Office Action, the Examiner rejects claims 25 and 31 under 35 U.S.C. § 112, second paragraph as allegedly being indefinite. The Examiner asserts that the scope and meaning of “80% identical” is unclear since the specification does not define the method by which percent identity is calculated. As a result, the Examiner alleges that it is unclear whether claim 25 reads on sequences that are shorter or longer than the instantly claimed 22-mer and share partial identity with it. Applicant respectfully disagrees.

Percent identity is used in the art to describe the degree of relatedness between two or more sequences. A description of the method of calculating percent identity would provide absolute precision to the scope. Absolute precision, however, is not required. *See, e.g., MPEP* § 2173.02 (“Some latitude in the manner of expression and the aptness of terms should be permitted even though the claim language is not as precise as the Examiner might desire.”) Instead, the relevant inquiry is whether claim language provides reasonable clarity to the scope of the claim by taking into account, for example, the teachings of the prior art and the claim interpretation by one of ordinary skill. *See MPEP* § 2173.02. In the art, percent identity is more often than not discussed without providing the method of calculation. As a result, Applicant respectfully submits that one of ordinary skill in the art would interpret the scope of claim 25, part (b) to include sequences both shorter and longer than SEQ ID NO: 7002375.

This is illustrated as follows. At its longest, the 80% variant of SEQ ID NO: 7002375 cannot exceed 27 nucleotides in length, as shown below.

SEQ ID NO: 7002375	ACATACACGGGAAACCTCTTTT
Example of longer 80% variant	ACATACACGGGAAACCTCTTTTNNNNN

This exemplary 80% variant of 27 nucleotides is 22/27, or 81.5% identical to SEQ ID NO: 7002375. If any other nucleotide of the 27-mer were to differ from SEQ ID NO: 7002375, it would be less than 80% identical to SEQ ID NO: 7002375.

On the other hand, at its shortest, again assuming that there is no nucleotide different between the 80% identical sequence and SEQ ID NO: 7002375, the 80% variant cannot be shorter than 18 nucleotides in length. This is exemplified below.

SEQ ID NO: 7002375 ACATACACGGGAAACCTCTTTT  
Example of shorter 80% variant ACATACACGGGAAACCTC  
where 18/22 = 81.8% identity

The exemplary 80% variant of 18 nucleotides is 81.8% identical to SEQ ID NO: 7002375. If any nucleotide of the 18-mer were to differ from SEQ ID NO: 7002375, it would be less than 80% identical to SEQ ID NO: 7002375. For either a shorter 80% variant or longer 80% variant, any nucleotide difference from SEQ ID NO: 7002375 would require that the variant be longer or shorter, respectively. Therefore, the 80% variant of part (a) in claim 25 must be 18-27 nucleotides in length.

For purposes of examination, however, the Examiner construes claim 25(b) broadly to include any sequence of any length comprising a sequence 80% identical to SEQ ID NO: 7002375. This interpretation by the Examiner leads to the inclusion of a 2941 nucleotide sequence that contains a 20 nucleotide stretch that is 95% identical to a portion of SEQ ID NO: 7002735. Applicant respectfully submits that the Examiner's interpretation is unreasonably broad and inconsistent with the usage of percent identity in the prior art and as appreciated by one of ordinary skill in art. *See MPEP* § 2173.02. One of ordinary skill would not view Examiner's example as a sequence 80% identical to SEQ ID NO: 7002735. In view of the foregoing, Applicant respectfully request that the Examiner reconsider and withdraw the rejection of claims 25 and 31 under 35 U.S.C. § 112, second paragraph.

**c. 35 U.S.C. § 102**

**(1) Over GenBank Accession No. BD247503.1**

On page 6 of the Office Action, the Examiner rejects claim 25 under 35 U.S.C. § 102(b) as allegedly being anticipated by GenBank Accession No. BD247503.1 (the “Maize Sequence”). The Maize sequence has a length of 2941 nucleotides and includes a twenty nucleotide stretch that is 95% identical to a portion of SEQ ID NO: 7002375. The Examiner asserts that the Maize Sequence comprises a sequence that is at least 80% identical to instant SEQ ID NO: 7002375. However, as described above, a proper interpretation of the scope of the claims excludes the Maize sequence. In view of the foregoing, Applicant respectfully requests that the Examiner reconsider and withdraw the rejection of the claim 25 under 35 U.S.C. § 102(b).

**(2) Over GenBank Access No. AC\_096504.7**

On page 7 of the Office Action, the Examiner rejects claims 25 and 31 under 35 U.S.C. § 102(b) as allegedly being anticipated by GenBank Accession No. AC\_096504.7 (the “Rat BAC”). The Rat BAC is at least 253,092 nucleotides in length and includes a sequence identical to SEQ ID NO: 7002375. The Examiner asserts that the Rat BAC in view of Kim *et al.* (1996) and the International Human genome Sequence Consortium (2001) (the “Cited 102 Reference”), taught a bacterial artificial chromosome vector containing a DNA encoding instant SEQ ID NO: 7002375. As described above, however, a proper interpretation of the claims excludes inserts such as that of the Rat BAC. In view of the foregoing remarks, Applicant respectfully requests that the Examiner reconsider and withdraw the rejection of the claims under 35 U.S.C. § 102(b).

**d. 35 U.S.C. § 103**

On pages 9-12 of the Office Action, the Examiner rejects claim 25 under 35 U.S.C. § 103(a) as allegedly being unpatentable over the Rat BAC in view of Buck *et al* (*BioTechniques*, 1999;27:528-36; “Buck”). The Examiner interprets the nucleic acid of parts (a), (c), and (d) of claim 25 to include DNA probes and sequencing primers. The Examiner contends that one of skill would have a reasonable expectation for a sequencing primer synthesized **essentially anywhere along a give sequence of interest** to perform adequately to yield sequence data. *The Office Action*, at p. 12. The Examiner thus concludes that it would have been obvious to one of skill to synthesize a DNA identical or complementary to instant SEQ ID NO: 7002375, or any sequence 80% identical to these sequences, as a primer in the process of determining the sequence of Rat BAC. *Id.*, at pages 11-12. Applicant respectfully disagrees.

Applicant submits that even if the primers cited by the Examiner include SEQ ID NO: 7002375 or its complement, this is not sufficient by itself to establish a *prima facie* case of obviousness. *See MPEP* §2144.08.II (“The fact that a claimed species or subgenus is encompassed by a prior art genus is not sufficient by itself to establish a *prima facie* case of obviousness”). Considering the massive size of the genus of sequences taught by Rat BAC in view of Buck, there is simply no way for one of skill to envisage the claimed subgenus of nucleic acids within the genus. *See MPEP* § 2144.08.a.4.(a). The Rat BAC insert is 253,092 nucleotides in length. Buck teaches design and generation of primers 17 to 24 nucleotides in length. *Buck*, at abstract. Accordingly, the group of 17 to 24 nucleotide-long primers cited by the Examiner that are capable of binding anywhere along the Rat BAC encompasses **at least 2,024,580 different sequences**. The claimed nucleic acid related to SEQ ID NO: 7002375 is but one subgenus within this massive genus of primers. There is no teaching or suggestion in the Rat BAC, the Cited 102 References, or Buck to lead one of skill to select a primer that is related to a miRNA, or any other sequence capable of regulating a gene transcript in *trans*, as is provided in the instant claims. The same holds true for probes—there is nothing in any of the art cited by the Examiner to lead one of skill to select

a probe related to SEQ ID NO: 7002375 from among over two million possible sequences taught by the Rat BAC sequence in view of Buck. In view of the foregoing remarks, the Applicant respectfully request that the Examiner reconsider and withdraw the rejection of claim 25 under 35 U.S.C. § 103(a).

### 3. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite the prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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